A. DAVENPORT          X 145.3

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          RAW SEQUENCE LISTING           DATE: 05/07/2001
          PATENT APPLICATION:  US/09/377,446   TIME: 13:56:33

          Input Set : N:\Crf3\RULE60\09377446.txt
          Output Set: N:\CRF3\05072001\I377446.raw

          SEQUENCE LISTING
  4 (1) GENERAL INFORMATION:
  6       (i) APPLICANT: Magal, Ella
  7                      Delaney, John M.
  9      (ii) TITLE OF INVENTION: METHOD FOR PREVENTING AND TREATING
 10                               HEARING LOSS USING A NEURTURIN PROTEIN PRODUCT
 12     (iii) NUMBER OF SEQUENCES: 5
 14      (iv) CORRESPONDENCE ADDRESS:
 15           (A) ADDRESSEE: Amgen Inc.
 16           (B) STREET: One Amgen Center Drive
 17           (C) CITY: Thousand Oaks
 18           (D) STATE: California
 19           (E) COUNTRY: USA
 20           (F) ZIP: 91320-1789
 22       (v) COMPUTER READABLE FORM:
 23           (A) MEDIUM TYPE: Floppy disk
 24           (B) COMPUTER: IBM PC compatible
 25           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 28      (vi) CURRENT APPLICATION DATA:
 29           (A) APPLICATION NUMBER: US/09/377,446
 30           (B) FILING DATE: 19-Aug-1999
 31           (C) CLASSIFICATION:
 33     (vii) PRIOR APPLICATION DATA:
 34           (A) APPLICATION NUMBER: 09/106,486
 35           (B) FILING DATE:
 37    (viii) ATTORNEY/AGENT INFORMATION:
 38           (A) NAME: Curry, Daniel R.
 39           (B) REGISTRATION NUMBER: 32,727
 40           (C) REFERENCE/DOCKET NUMBER: A-444
 43 (2) INFORMATION FOR SEQ ID NO: 1:
 45       (i) SEQUENCE CHARACTERISTICS:
 46           (A) LENGTH: 102 amino acids
 47           (B) TYPE: amino acid
 48           (C) STRANDEDNESS: single
 49           (D) TOPOLOGY: linear
 51      (ii) MOLECULE TYPE: protein
 56      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 58      Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
 59      1               5                   10                  15
 61      Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
 62                  20                  25                  30
 64      Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
 65              35                  40                  45
 67      Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
 68          50                  55                  60
 70      Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
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C--> 29
C--> 30

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 71        65                    70                    75                    80
 73·       Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 74                      85                    90                    95
 76        Arg Glu Cys Ala Cys Val
 77                       100
 79 (2) INFORMATION FOR SEQ ID NO: 2:
 81        (i) SEQUENCE CHARACTERISTICS:
 82            (A) LENGTH: 100 amino acids
 83            (B) TYPE: amino acid
 84            (C) STRANDEDNESS: single
 85            (D) TOPOLOGY: linear
 87       (ii) MOLECULE TYPE: protein
 92       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 94        Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 95        1               5                   10                  15
 97        Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 98                      20                    25                    30
100        Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
101                  35                    40                    45
103        Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
104              50                    55                    60
106        His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
107        65                    70                    75                    80
109        Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
110                      85                    90                    95
112        Cys Ala Cys Val
113                  100
115 (2) INFORMATION FOR SEQ ID NO: 3:
117        (i) SEQUENCE CHARACTERISTICS:
118            (A) LENGTH: 312 base pairs
119            (B) TYPE: nucleic acid
120            (C) STRANDEDNESS: single
121            (D) TOPOLOGY: linear
123       (ii) MOLECULE TYPE: DNA (genomic)
126       (ix) FEATURE:
127            (A) NAME/KEY: CDS
128            (B) LOCATION: 1..309
131       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
133 ATG GCA CGT CTG GGT GCT CGT CCG TGT GGT CTG CGT GAA CTG GAA GTT        48
134 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
135  1               5                   10                  15
137 CGT GTT TCC GAA CTG GGT CTG GGT TAC GCT TCC GAC GAA ACC GTT CTG        96
138 Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
139             20                    25                    30
141 TTC CGT TAC TGT GCA GGT GCT TGT GAA GCA GCT GCA CGT GTT TAC GAC       144
142 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
143         35                    40                    45
145 CTG GGT CTG CGT CGC CTG CGT CAG CGC CGT CGC CTG CGT CGC GAA CGT       192
146 Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
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147      50                 55                 60
149 GTT CGC GCA CAG CCG TGT TGC CGT CCG ACC GCA TAC GAA GAC GAA GTT          240
150 Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
151   65                 70                 75                 80
153 TCC TTC CTG GAC GCT CAC TCC CGT TAC CAC ACC GTT CAC GAA CTG TCC          288
154 Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
155                 85                 90                 95
157 GCA CGT CAC TGT GCG TGT GTT TAA                                          312
158 Ala Arg His Cys Ala Cys Val
159             100
162 (2) INFORMATION FOR SEQ ID NO: 4:
164      (i) SEQUENCE CHARACTERISTICS:
165          (A) LENGTH: 103 amino acids
166          (B) TYPE: amino acid
167          (D) TOPOLOGY: linear
169     (ii) MOLECULE TYPE: protein
171     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
173 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
174   1                 5                 10                 15
176 Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
177                 20                 25                 30
179 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
180             35                 40                 45
182 Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
183       50                 55                 60
185 Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
186   65                 70                 75                 80
188 Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
189                 85                 90                 95
191 Ala Arg His Cys Ala Cys Val
192             100
194 (2) INFORMATION FOR SEQ ID NO: 5:
196      (i) SEQUENCE CHARACTERISTICS:
197          (A) LENGTH: 197 amino acids
198          (B) TYPE: amino acid
199          (C) STRANDEDNESS: single
200          (D) TOPOLOGY: linear
202     (ii) MOLECULE TYPE: protein
207     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
209     Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
210     1                 5                 10                 15
212     Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
213                 20                 25                 30
215     Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
216             35                 40                 45
218     Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
219         50                 55                 60
221     Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
222     65                 70                 75                 80
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